

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/757,843A
Source: IFW0
Date Processed by STIC: 3/2/05

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IFWO

RAW SEQUENCE LISTING

DATE: 03/02/2005

PATENT APPLICATION: US/10/757,843A

TIME: 10:19:15

Input Set : D:\PHOE0188.ST25.txt

Output Set: N:\CRF4\03022005\J757843A.raw

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3 <110> APPLICANT: Clark, Mike A.
5 <120> TITLE OF INVENTION: MODIFIED ARGININE DEIMINASE
7 <130> FILE REFERENCE: PHOE-0188
9 <140> CURRENT APPLICATION NUMBER: US 10/757,843A
10 <141> CURRENT FILING DATE: 2004-01-15
12 <150> PRIOR APPLICATION NUMBER: US 09/723,546
13 <151> PRIOR FILING DATE: 2000-11-28
15 <150> PRIOR APPLICATION NUMBER: US 09/023,809
16 <151> PRIOR FILING DATE: 1998-02-13
18 <150> PRIOR APPLICATION NUMBER: US 60/046,200
19 <151> PRIOR FILING DATE: 1997-05-12
21 <160> NUMBER OF SEQ ID NOS: 14
23 <170> SOFTWARE: PatentIn version 3.3
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 410
27 <212> TYPE: PRT
28 <213> ORGANISM: Mycoplasma arginini
30 <400> SEQUENCE: 1
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36 Ile Gly Glu Leu Glu Ser Val Leu Val His Glu Pro Gly Arg Glu Ile
37 20 25 30
40 Asp Tyr Ile Thr Pro Ala Arg Leu Asp Glu Leu Leu Phe Ser Ala Ile
41 35 40 45
44 Leu Glu Ser His Asp Ala Arg Lys Glu His Lys Gln Phe Val Ala Glu
45 50 55 60
48 Leu Lys Ala Asn Asp Ile Asn Val Val Glu Leu Ile Asp Leu Val Ala
49 65 70 75 80
52 Glu Thr Tyr Asp Leu Ala Ser Gln Glu Ala Lys Asp Lys Leu Ile Glu
53 85 90 95
56 Glu Phe Leu Glu Asp Ser Glu Pro Val Leu Ser Glu Glu His Lys Val
57 100 105 110
60 Val Val Arg Asn Phe Leu Lys Ala Lys Lys Thr Ser Arg Lys Leu Val
61 115 120 125
64 Glu Ile Met Met Ala Gly Ile Thr Lys Tyr Asp Leu Gly Ile Glu Ala
65 130 135 140
68 Asp His Glu Leu Ile Val Asp Pro Met Pro Asn Leu Tyr Phe Thr Arg
69 145 150 155 160
72 Asp Pro Phe Ala Ser Val Gly Asn Gly Val Thr Ile His Tyr Met Arg
73 165 170 175
76 Tyr Lys Val Arg Gln Arg Glu Thr Leu Phe Ser Arg Phe Val Phe Ser
77 180 185 190
80 Asn His Pro Lys Leu Ile Asn Thr Pro Trp Tyr Tyr Asp Pro Ser Leu

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84 Lys Leu Ser Ile Glu Gly Gly Asp Val Phe Ile Tyr Asn Asn Asp Thr
85          210          215          220
88 Leu Val Val Gly Val Ser Glu Arg Thr Asp Leu Gln Thr Val Thr Leu
89 225          230          235          240
92 Leu Ala Lys Asn Ile Val Ala Asn Lys Glu Cys Glu Phe Lys Arg Ile
93          245          250          255
96 Val Ala Ile Asn Val Pro Lys Trp Thr Asn Leu Met His Leu Asp Thr
97          260          265          270
100 Trp Leu Thr Met Leu Asp Lys Asp Lys Phe Leu Tyr Ser Pro Ile Ala
101          275          280          285
104 Asn Asp Val Phe Lys Phe Trp Asp Tyr Asp Leu Val Asn Gly Gly Ala
105          290          295          300
108 Glu Pro Gln Pro Val Glu Asn Gly Leu Pro Leu Glu Gly Leu Leu Gln
109 305          310          315          320
112 Ser Ile Ile Asn Lys Lys Pro Val Leu Ile Pro Ile Ala Gly Glu Gly
113          325          330          335
116 Ala Ser Gln Met Glu Ile Glu Arg Glu Thr His Phe Asp Gly Thr Asn
117          340          345          350
120 Tyr Leu Ala Ile Arg Pro Gly Val Ile Gly Tyr Ser Arg Asn Glu
121          355          360          365
124 Lys Thr Asn Ala Ala Leu Glu Ala Ala Gly Ile Lys Val Leu Pro Phe
125          370          375          380
128 His Gly Asn Gln Leu Ser Leu Gly Met Gly Asn Ala Arg Cys Met Ser
129 385          390          395          400
132 Met Pro Leu Ser Arg Lys Asp Val Lys Trp
133          405          410
136 <210> SEQ ID NO: 2
137 <211> LENGTH: 410
138 <212> TYPE: PRT
139 <213> ORGANISM: Mycoplasma arthritides
141 <400> SEQUENCE: 2
143 Met Ser Val Phe Asp Ser Lys Phe Lys Gly Ile His Val Tyr Ser Glu
144 1          5          10          15
147 Ile Gly Glu Leu Glu Ser Val Leu Val His Glu Pro Gly Arg Glu Ile
148          20          25          30
151 Asp Tyr Ile Thr Pro Ala Arg Leu Asp Glu Leu Leu Phe Ser Ala Ile
152          35          40          45
155 Leu Glu Ser His Asp Ala Arg Lys Glu Gln Ser Gln Phe Val Ala Ile
156          50          55          60
159 Leu Lys Ala Asn Asp Ile Asn Val Val Glu Thr Ile Asp Leu Val Ala
160 65          70          75          80
163 Glu Thr Tyr Asp Leu Ala Ser Gln Glu Ala Lys Asp Arg Leu Ile Glu
164          85          90          95
167 Glu Phe Leu Glu Asp Ser Glu Pro Val Leu Ser Glu Ala His Lys Lys
168          100          105          110
171 Val Val Arg Asn Phe Leu Lys Ala Lys Lys Thr Ser Arg Lys Leu Val
172          115          120          125
175 Glu Leu Met Met Ala Gly Ile Thr Lys Tyr Asp Leu Gly Val Glu Ala

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176      130      135      140
179 Asp His Glu Leu Ile Val Asp Pro Met Pro Asn Leu Tyr Phe Thr Arg
180 145      150      155      160
183 Asp Pro Phe Ala Ser Val Gly Asn Gly Val Thr Ile His Phe Met Arg
184      165      170      175
187 Tyr Lys Val Arg Arg Arg Glu Thr Leu Phe Ser Arg Phe Val Phe Arg
188      180      185      190
191 Asn His Pro Lys Leu Val Asn Thr Pro Trp Tyr Tyr Asp Pro Ala Met
192      195      200      205
195 Lys Leu Ser Ile Glu Gly Gly Asp Val Phe Ile Tyr Asn Asn Asp Thr
196      210      215      220
199 Leu Val Val Gly Val Ser Glu Arg Thr Asp Leu Asp Thr Val Thr Leu
200 225      230      235      240
203 Leu Ala Lys Asn Leu Val Ala Asn Lys Glu Cys Glu Phe Lys Arg Ile
204      245      250      255
207 Val Ala Ile Asn Val Pro Lys Trp Thr Asn Leu Met His Leu Asp Thr
208      260      265      270
211 Trp Leu Thr Met Leu Asp Lys Asn Lys Phe Leu Tyr Ser Pro Ile Ala
212      275      280      285
215 Asn Asp Val Phe Lys Phe Trp Asp Tyr Asp Leu Val Asn Gly Gly Ala
216      290      295      300
219 Glu Pro Gln Pro Val Glu Asn Gly Leu Pro Leu Glu Lys Leu Leu Gln
220 305      310      315      320
223 Ser Ile Ile Asn Lys Lys Pro Val Leu Ile Pro Ile Ala Gly Glu Gly
224      325      330      335
227 Ala Ser Gln Met Glu Ile Glu Arg Glu Thr His Phe Asp Gly Thr Asn
228      340      345      350
231 Tyr Ile Ala Ile Arg Pro Gly Val Val Ile Gly Tyr Ser Arg Asn Glu
232      355      360      365
235 Lys Thr Asn Ala Ala Leu Lys Ala Ala Gly Ile Lys Val Leu Pro Phe
236      370      375      380
239 His Gly Asn Gln Leu Ser Leu Gly Met Gly Asn Ala Arg Cys Met Ser
240 385      390      395      400
243 Met Pro Leu Ser Arg Lys Asp Val Lys Trp
244      405      410
247 <210> SEQ ID NO: 3
248 <211> LENGTH: 409
249 <212> TYPE: PRT
250 <213> ORGANISM: Mycoplasma hominus
252 <400> SEQUENCE: 3
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255 1      5      10      15
258 Ile Gly Glu Leu Glu Thr Val Leu Val His Glu Pro Gly Arg Glu Ile
259      20      25      30
262 Asp Tyr Ile Thr Pro Ala Arg Leu Asp Glu Leu Leu Phe Ser Ala Ile
263      35      40      45
266 Leu Glu Ser His Asp Ala Arg Lys Glu His Gln Ser Phe Val Lys Ile
267      50      55      60
270 Met Lys Asp Arg Gly Ile Asn Val Val Glu Leu Thr Asp Leu Val Ala

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271 65          70          75          80
274 Glu Thr Tyr Asp Leu Ala Ser Lys Ala Ala Lys Glu Glu Phe Ile Glu
275          85          90          95
278 Thr Phe Leu Glu Glu Thr Val Pro Val Leu Thr Glu Ala Asn Lys Lys
279          100          105          110
282 Ala Val Arg Ala Phe Leu Leu Ser Lys Pro Thr His Glu Met Val Glu
283          115          120          125
286 Phe Met Met Ser Gly Ile Thr Lys Tyr Glu Leu Gly Val Glu Ser Glu
287          130          135          140
290 Asn Glu Leu Ile Val Asp Pro Met Pro Asn Leu Tyr Phe Thr Arg Asp
291 145          150          155          160
294 Pro Phe Ala Ser Val Gly Asn Gly Val Thr Ile His Phe Met Arg Tyr
295          165          170          175
298 Ile Val Arg Arg Arg Glu Thr Leu Phe Ala Arg Phe Val Phe Arg Asn
299          180          185          190
302 His Pro Lys Leu Val Lys Thr Pro Trp Tyr Tyr Asp Pro Ala Met Lys
303          195          200          205
306 Met Pro Ile Glu Gly Gly Asp Val Phe Ile Tyr Asn Asn Glu Thr Leu
307          210          215          220
310 Val Val Gly Val Ser Glu Arg Thr Asp Leu Asp Thr Ile Thr Leu Leu
311 225          230          235          240
314 Ala Lys Asn Ile Lys Ala Asn Lys Glu Val Glu Phe Lys Arg Ile Val
315          245          250          255
318 Ala Ile Asn Val Pro Lys Trp Thr Asn Leu Met His Leu Asp Thr Trp
319          260          265          270
322 Leu Thr Met Leu Asp Lys Asn Lys Phe Leu Tyr Ser Pro Ile Ala Asn
323          275          280          285
326 Asp Val Phe Lys Phe Trp Asp Tyr Asp Leu Val Asn Gly Gly Ala Glu
327          290          295          300
330 Pro Gln Pro Gln Leu Asn Gly Leu Pro Leu Asp Lys Leu Leu Ala Ser
331 305          310          315          320
334 Ile Ile Asn Lys Glu Pro Val Leu Ile Pro Ile Gly Gly Ala Gly Ala
335          325          330          335
338 Thr Glu Met Glu Ile Ala Arg Glu Thr Asn Phe Asp Gly Thr Asn Tyr
339          340          345          350
342 Leu Ala Ile Lys Pro Gly Leu Val Ile Gly Tyr Asp Arg Asn Glu Lys
343          355          360          365
346 Thr Asn Ala Ala Leu Lys Ala Ala Gly Ile Thr Val Leu Pro Phe His
347          370          375          380
350 Gly Asn Gln Leu Ser Leu Gly Met Gly Asn Ala Arg Cys Met Ser Met
351 385          390          395          400
354 Pro Leu Ser Arg Lys Asp Val Lys Trp
355          405
358 <210> SEQ ID NO: 4
359 <211> LENGTH: 25
360 <212> TYPE: DNA
361 <213> ORGANISM: Mycoplasma arginini
363 <400> SEQUENCE: 4
364 gggatccatg tctgtatttg acagt

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368 <211> LENGTH: 33
369 <212> TYPE: DNA
370 <213> ORGANISM: Mycoplasma arginini
372 <400> SEQUENCE: 5
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376 <210> SEQ ID NO: 6
377 <211> LENGTH: 411
378 <212> TYPE: PRT
379 <213> ORGANISM: Streptococcus pyogenes
381 <400> SEQUENCE: 6
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384 1 5 10 15
387 Lys Lys Val Leu Leu His Arg Pro Gly Lys Glu Ile Glu Asn Leu Met
388 20 25 30
391 Pro Asp Tyr Leu Glu Arg Leu Leu Phe Asp Asp Ile Pro Phe Leu Glu
392 35 40 45
395 Asp Ala Gln Lys Glu His Asp Ala Phe Ala Gln Ala Leu Arg Asp Glu
396 50 55 60
399 Gly Ile Glu Val Leu Tyr Leu Glu Thr Leu Ala Ala Glu Ser Leu Val
400 65 70 75 80
403 Thr Pro Glu Ile Arg Glu Ala Phe Ile Asp Glu Tyr Leu Ser Glu Ala
404 85 90 95
407 Asn Ile Arg Gly Arg Ala Thr Lys Lys Ala Ile Arg Glu Leu Leu Met
408 100 105 110
411 Ala Ile Glu Asp Asn Gln Glu Leu Ile Glu Lys Thr Met Ala Gly Val
412 115 120 125
415 Gln Lys Ser Glu Leu Pro Glu Ile Pro Ala Ser Glu Lys Gly Leu Thr
416 130 135 140
419 Asp Leu Val Glu Ser Asn Tyr Pro Phe Ala Ile Asp Pro Met Pro Asn
420 145 150 155 160
423 Leu Tyr Phe Thr Arg Asp Pro Phe Ala Thr Ile Gly Thr Gly Val Ser
424 165 170 175
427 Leu Asn His Met Phe Ser Glu Thr Arg Asn Arg Glu Thr Leu Tyr Gly
428 180 185 190
431 Lys Tyr Ile Phe Thr His His Pro Ile Tyr Gly Gly Gly Lys Val Pro
432 195 200 205
435 Met Val Tyr Asp Arg Asn Glu Thr Thr Arg Ile Glu Gly Gly Asp Glu
436 210 215 220
439 Leu Val Leu Ser Lys Asp Val Leu Ala Val Gly Ile Ser Gln Arg Thr
440 225 230 235 240
443 Asp Ala Ala Ser Ile Glu Lys Leu Leu Val Asn Ile Phe Lys Gln Asn
444 245 250 255
447 Leu Gly Phe Lys Lys Val Leu Ala Phe Glu Phe Ala Asn Asn Arg Lys
448 260 265 270
451 Phe Met His Leu Asp Thr Val Phe Thr Met Val Asp Tyr Asp Lys Phe
452 275 280 285
455 Thr Ile His Pro Glu Ile Glu Gly Asp Leu Arg Val Tyr Ser Val Thr
456 290 295 300

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VERIFICATION SUMMARY

DATE: 03/02/2005

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Input Set : D:\PHOE0188.ST25.txt

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